

Input Set: I512363.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: Ni, Jian  
2 Ruben, Steven M.  
3 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins  
4 TR11, TR11SV1, and TR11SV2  
5 <130> FILE REFERENCE: PF396  
6 <140> CURRENT APPLICATION NUMBER: US/09/512,363  
7 <141> CURRENT FILING DATE: 2000-02-23  
8 <150> EARLIER APPLICATION NUMBER: 60/063,212  
9 <151> EARLIER FILING DATE: 1997-10-21  
10 <150> EARLIER APPLICATION NUMBER: 09/176,200  
11 <151> EARLIER FILING DATE: 1998-10-21  
12 <150> EARLIER APPLICATION NUMBER: 60/121,648  
13 <151> EARLIER FILING DATE: 1999-02-24  
14 <150> EARLIER APPLICATION NUMBER: 60/134,172  
15 <151> EARLIER FILING DATE: 1999-05-13  
16 <150> EARLIER APPLICATION NUMBER: 60/144,076  
17 <151> EARLIER FILING DATE: 1999-07-16  
18 <160> NUMBER OF SEQ ID NOS: 28  
19 <170> SOFTWARE: PatentIn Ver. 2.0  
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21 <211> LENGTH: 983  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
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25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (118)..(819)  
27 <220> FEATURE:  
28 <221> NAME/KEY: mat\_peptide  
29 <222> LOCATION: (193)..(819)  
30 <220> FEATURE:  
31 <221> NAME/KEY: scRNA  
32 <222> LOCATION: (118)..(192)  
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35 cgggtgagga cggggacggg gcgtgtccaa ctggctgtgg gctttgaaa cccgagc 117  
36 atg gca cag cac ggg gcg atg ggc gcg ttt cgg gcc ctg tgc ggc ctg 165  
37 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu  
38 -25 -20 -15 -10  
39 gcg ctg ctg tgc gcg ctc agc ctg ggt cag cgc ccc acc ggg ggt ccc 213  
40 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro  
41 -5 -1 1 5  
42 ggg tgc ggc cct ggg cgc ctc ctg ctt ggg acg gga acg gac gcg cgc 261  
43 Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg  
44 10 15 20

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45 tgc tgc cgg gtt cac acg acg cgc tgc tgc cgc gat tac ccg ggc gag 309  
46 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu  
47 25 30 35  
48 gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac 357  
49 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
50 40 45 50 55  
51 tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca 405  
52 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro  
53 60 65 70  
54 ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt 453  
55 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
56 75 80 85  
57 atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc 501  
58 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
59 90 95 100  
60 aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct 549  
61 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
62 105 110 115  
63 ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca 597  
64 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
65 120 125 130 135  
66 gag ccg ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc 645  
67 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
68 140 145 150  
69 gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg 693  
70 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
71 155 160 165  
72 agg aag acc cag ctg ctg gag gtg ccg ccg tcg acc gaa gac gcc 741  
73 Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala  
74 170 175 180  
75 aga agc tgc cag ttc ccc gag gaa gag cgg ggc gag cga tcg gca gag 789  
76 Arg Ser Cys Gln Phe Pro Glu Glu Arg Gly Glu Arg Ser Ala Glu  
77 185 190 195  
78 gag aag ggg cgg ctg gga gac ctg tgg gtg tgagcctggc cgtcctccgg 839  
79 Glu Lys Gly Arg Leu Gly Asp Leu Trp Val  
80 200 205  
81 ggccaccgac cgccaggccccc ccctccccag gagctccccca ggccgcagg gctctgcgtt 899  
82 ctgctctggg ccggggccctg ctccccctggc agcagaagtg ggtgcaggaa ggtggcactg 959  
83 accagcgccc tgaccatgc agtt 983  
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85 <211> LENGTH: 234  
86 <212> TYPE: PRT  
87 <213> ORGANISM: Homo sapiens  
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90 -25 -20 -15 -10  
91 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro  
92 -5 -1 1 5  
93 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg  
94 10 15 20

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95 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu  
96 25 30 35  
97 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
98 40 45 50 55  
99 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro  
100 60 65 70  
101 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
102 75 80 85  
103 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
104 90 95 100  
105 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
106 105 110 115  
107 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
108 120 125 130 135  
109 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
110 140 145 150  
111 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
112 155 160 165  
113 Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala  
114 170 175 180  
115 Arg Ser Cys Gln Phe Pro Glu Glu Arg Gly Glu Arg Ser Ala Glu  
116 185 190 195  
117 Glu Lys Gly Arg Leu Gly Asp Leu Trp Val  
118 200 205

119 <210> SEQ ID NO 3

120 <211> LENGTH: 1007

121 <212> TYPE: DNA

122 <213> ORGANISM: Homo sapiens

123 <220> FEATURE:

124 <221> NAME/KEY: CDS

125 <222> LOCATION: (121)..(843)

126 <400> SEQUENCE: 3

127 gtcgaccac gctgtccgggg ggccacccct gggtcctgca ggggcagctc ctggttgcat 60  
128 atggaggtag cacctggca gggcagctg tggggcgcaa agggggagta gccaggccac 120  
129 atg gcc cca gga gaa aga gac agc tgg ata aac cca ggt cca gac tcc 168  
130 Met Ala Pro Gly Glu Arg Asp Ser Trp Ile Asn Pro Gly Pro Asp Ser  
131 1 5 10 15  
132 cag cca gga gcc ctc tgc tcc ctg gag cca act gtg ggt gga gaa cgg 216  
133 Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg  
134 20 25 30  
135 aca acc tca ctc ccc tgg agg gcc gag ggg agg cct ggg gag gag ggg 264  
136 Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Gly  
137 35 40 45  
138 gcc tca gcc cag ctg ctg ggg ggc tgg cct gtc tcc tgc cca ggc gag 312  
139 Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu  
140 50 55 60  
141 gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac 360  
142 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
143 65 70 75 80  
144 tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca 408

Input Set: I512363.RAW

145 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro  
 146 85 90 95  
 147 ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt 456  
 148 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
 149 100 105 110  
 150 atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc 504  
 151 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
 152 115 120 125  
 153 aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct 552  
 154 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
 155 130 135 140  
 156 ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca 600  
 157 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
 158 145 150 155 160  
 159 gag ccc ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc 648  
 160 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
 161 165 170 175  
 162 gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg 696  
 163 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
 164 180 185 190  
 165 agg agt cag tgc atg tgg ccc cga gag acc cag ctg ctg ctg gag gtg 744  
 166 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val  
 167 195 200 205  
 168 ccg ccg tcg acc gaa gac gcc aga agc tgc cag ttc ccc gag gaa gag 792  
 169 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu  
 170 210 215 220  
 171 cggtggc gag cga tcg gca gag gag aag ggg cgg ctg gga gac ctg tgg 840  
 172 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp  
 173 225 230 235 240  
 174 gtgtgagccctggc cgtccctccgg ggccaccgac cgcagccagc ccctccccag 893  
 175 Val

W--&gt;

176  
 177 gagctccccca ggccgcagg gctctgcgtt ctgctctggg ccggggccctg ctccccctggc 953  
 178 agcagaagtg ggtgcaggaa ggtggcagtg accagcgccc tggaccatgc agtt 1007  
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 180 <211> LENGTH: 241  
 181 <212> TYPE: PRT  
 182 <213> ORGANISM: Homo sapiens  
 183 <400> SEQUENCE: 4  
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 185 1 5 10 15  
 186 Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg  
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 188 Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Glu Gly  
 189 35 40 45  
 190 Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu  
 191 50 55 60  
 192 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
 193 65 70 75 80  
 194 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro

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195                        85                        90                        95  
 196 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
 197                        100                        105                        110  
 198 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
 199                        115                        120                        125  
 200 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
 201                        130                        135                        140  
 202 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
 203                        145                        150                        155                        160  
 204 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
 205                        165                        170                        175  
 206 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
 207                        180                        185                        190  
 208 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val  
 209                        195                        200                        205  
 210 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu  
 211                        210                        215                        220  
 212 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp  
 213                        225                        230                        235                        240  
 214 Val  
 215 <210> SEQ ID NO 5  
 216 <211> LENGTH: 1074  
 217 <212> TYPE: DNA  
 218 <213> ORGANISM: Homo sapiens  
 219 <220> FEATURE:  
 220 <221> NAME/KEY: CDS  
 221 <222> LOCATION: (1)..(720)  
 222 <220> FEATURE:  
 223 <221> NAME/KEY: sig\_peptide  
 224 <222> LOCATION: (1)..(57)  
 225 <220> FEATURE:  
 226 <221> NAME/KEY: mat\_peptide  
 227 <222> LOCATION: (58)..(720)  
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 230 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu  
 231                        -15                        -10                        -5  
 232 agc ctg ggt cag cgc ccc acc ggg ggt ccc ggg tgc ggc cct ggg cgc      96  
 233 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg  
 234                        -1                        1                        5                                10  
 235 ctc ctg ctt ggg acg gga acg gac gcg cgc tgc tgc cgg gtt cac acg      144  
 236 Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr  
 237                        15                        20                        25  
 238 acg cgc tgc tgc cgc gat tac ccg gcc cag ctg ctg ggg ggc tgg cct      192  
 239 Thr Arg Cys Cys Arg Asp Tyr Pro Ala Gln Leu Leu Gly Gly Trp Pro  
 240                        30                        35                        40                        45  
 241 gtc tcc tgc cca ggc gag gag tgc tgt tcc gag tgg gac tgc atg tgt      240  
 242 Val Ser Cys Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met Cys  
 243                        50                        55                        60  
 244 gtc cag cct gaa ttc cac tgc gga gac cct tgc tgc acg acc tgc cgg      288

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I512363.RAW

Line	?	Error/Warning	Original Text
176	W	Invalid/Missing Amino Acid Numbering	
384	W	"N" or "Xaa" used: Feature required	cgattAACCC ggggcgaaga atngtggtt ccgagtn
385	W	"N" or "Xaa" used: Feature required	gccttgaat tccaattgcg gaagaaccct tngctgc
386	W	"N" or "Xaa" used: Feature required	acctttgttc ccccaaAGCC naagggggta anaattcc
452	W	"N" or "Xaa" used: Feature required	ggccgagggg aggcctgggg aggagggggc ctcagccc
453	W	"N" or "Xaa" used: Feature required	ctcctgccc ggcgaggant gctgttccga gtggaaat
454	W	"N" or "Xaa" used: Feature required	ccattgcga gaaccttgct gcacgaattt ccggcaac
455	W	"N" or "Xaa" used: Feature required	ggttnacattt ccaggggaaan ttcatTTTT gnttccat
456	W	"N" or "Xaa" used: Feature required	ttntccgggg gccanaaggc aatgaaaaac ttgganaa
457	W	"N" or "Xaa" used: Feature required	ttccnngggaa aagaccanaa gtttttggtc caggtccc

Input Set: I512363.RAW

## PREVIOUSLY ERRORED SEQUENCES-EDITED

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1 <210> 28  
2 <211> 241  
3 <212> PRT  
4 <213> Homo sapiens  
5 <400> 28  
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7 1 5 10 15  
8 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro  
9 20 25 30  
10 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg  
11 35 40 45  
12 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu  
13 50 55 60  
14 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
15 65 70 75 80  
16 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro  
17 85 90 95  
18 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
19 100 105 110  
20 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
21 115 120 125  
22 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
23 130 135 140  
24 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
25 145 150 155 160  
26 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
27 165 170 175  
28 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
29 180 185 190  
30 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val  
31 195 200 205  
32 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu  
33 210 215 220  
34 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp  
35 225 230 235 240  
36 Val